

SEQUENCE LISTING

<110> Yasuhiko MUNAKATA et al.

<120> Novel human parvovirus B19 receptor and uses thereof

<130>

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<211> 732

<212> PRT

10 <213> Homo sapiens

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35 40 45

Glu Asn Lys Asp Glu Ile Ala Leu Val Leu Phe Gly Thr Asp Gly Thr

50 55 60

20 Asp Asn Pro Leu Ser Gly Gly Asp Gln Tyr Gln Asn Ile Thr Val His

65 70 75 80

Arg His Leu Met Leu Pro Asp Phe Asp Leu Leu Glu Asp Ile Glu Ser

85 90 95

Lys Ile Gln Pro Gly Ser Gln Gln Ala Asp Phe Leu Asp Ala Leu Ile

25 100 105 110

Val Ser Met Asp Val Ile Gln His Glu Thr Ile Gly Lys Lys Phe Glu

115 120 125

Lys Arg His Ile Glu Ile Phe Thr Asp Leu Ser Ser Arg Phe Ser Lys
 130 135 140
 Ser Gln Leu Asp Ile Ile Ile His Ser Leu Lys Lys Cys Asp Ile Ser
 145 150 155 160
 5 Leu Gln Phe Phe Leu Pro Phe Ser Leu Gly Lys Glu Asp Gly Ser Gly
 165 170 175
 Asp Arg Gly Asp Gly Pro Phe Arg Leu Gly Gly His Gly Pro Ser Phe
 180 185 190
 Pro Leu Lys Gly Ile Thr Glu Gln Gln Lys Glu Gly Leu Glu Ile Val
 10 195 200 205
 Lys Met Val Met Ile Ser Leu Glu Gly Glu Asp Gly Leu Asp Glu Ile
 210 215 220
 Tyr Ser Phe Ser Glu Ser Leu Arg Lys Leu Cys Val Phe Lys Lys Ile
 225 230 235 240
 15 Glu Arg His Ser Ile His Trp Pro Cys Arg Leu Thr Ile Gly Ser Asn
 245 250 255
 Leu Ser Ile Arg Ile Ala Ala Tyr Lys Ser Ile Leu Gln Glu Arg Val
 260 265 270
 Lys Lys Thr Trp Thr Val Val Asp Ala Lys Thr Leu Lys Lys Glu Asp
 20 275 280 285
 Ile Gln Lys Glu Thr Val Tyr Cys Leu Asn Asp Asp Asp Glu Thr Glu
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 Val Leu Lys Glu Asp Ile Ile Gln Gly Phe Arg Tyr Gly Ser Asp Ile
 305 310 315 320
 25 Val Pro Phe Ser Lys Val Asp Glu Glu Gln Met Lys Tyr Lys Ser Glu
 325 330 335
 Gly Lys Cys Phe Ser Val Leu Gly Phe Cys Lys Ser Ser Gln Val Gln

	340	345	350
	Arg Arg Phe Phe Met Gly Asn Gln Val Leu Lys Val Phe Ala Ala Arg		
	355	360	365
	Asp Asp Glu Ala Ala Ala Val Ala Leu Ser Ser Leu Ile His Ala Leu		
5	370	375	380
	Asp Asp Leu Asp Met Val Ala Ile Val Arg Tyr Ala Tyr Asp Lys Arg		
	385	390	395
	Ala Asn Pro Gln Val Gly Val Ala Phe Pro His Ile Lys His Asn Tyr		
	405	410	415
10	Glu Cys Leu Val Tyr Val Gln Leu Pro Phe Met Glu Asp Leu Arg Gln		
	420	425	430
	Tyr Met Phe Ser Ser Leu Lys Asn Ser Lys Lys Tyr Ala Pro Thr Glu		
	435	440	445
	Ala Gln Leu Asn Ala Val Asp Ala Leu Ile Asp Ser Met Ser Leu Ala		
15	450	455	460
	Lys Lys Asp Glu Lys Thr Asp Thr Leu Glu Asp Leu Phe Pro Thr Thr		
	465	470	475
	480		
	Lys Ile Pro Asn Pro Arg Phe Gln Arg Leu Phe Gln Cys Leu Leu His		
	485	490	495
20	Arg Ala Leu His Pro Arg Glu Pro Leu Pro Pro Ile Gln Gln His Ile		
	500	505	510
	Trp Asn Met Leu Asn Pro Pro Ala Glu Val Thr Thr Lys Ser Gln Ile		
	515	520	525
	Pro Leu Ser Lys Ile Lys Thr Leu Phe Pro Leu Ile Glu Ala Lys Lys		
25	530	535	540
	Lys Asp Gln Val Thr Ala Gln Glu Ile Phe Gln Asp Asn His Glu Asp		
	545	550	555
	560		

Gly Pro Thr Ala Lys Lys Leu Lys Thr Glu Gln Gly Gly Ala His Phe
 565 570 575
 Ser Val Ser Ser Leu Ala Glu Gly Ser Val Thr Ser Val Gly Ser Val
 580 585 590
 5 Asn Pro Ala Glu Asn Phe Arg Val Leu Val Lys Gln Lys Lys Ala Ser
 595 600 605
 Phe Glu Glu Ala Ser Asn Gln Leu Ile Asn His Ile Glu Gln Phe Leu
 610 615 620
 Asp Thr Asn Glu Thr Pro Tyr Phe Met Lys Ser Ile Asp Cys Ile Arg
 10 625 630 635 640
 Ala Phe Arg Glu Glu Ala Ile Lys Phe Ser Glu Glu Gln Arg Phe Asn
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 Asn Phe Leu Lys Ala Leu Gln Glu Lys Val Glu Ile Lys Gln Leu Asn
 660 665 670
 15 His Phe Trp Glu Ile Val Val Gln Asp Gly Ile Thr Leu Ile Thr Lys
 675 680 685
 Glu Glu Ala Ser Gly Ser Ser Val Thr Ala Glu Glu Ala Lys Lys Phe
 690 695 700
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<212> DNA

<213> Homo sapiens

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 Val Val Leu Cys Met Asp Val Gly Phe Thr Met Ser Asn Ser Ile Pro

10 15 20 25

10 ggt ata gaa tcc cca ttt gaa caa gca aag aag gtg ata acc atg ttt 150
 Gly Ile Glu Ser Pro Phe Glu Gln Ala Lys Lys Val Ile Thr Met Phe

30 35 40

15 gta cag cga cag gtg ttt gct gag aac aag gat gag att gct tta gtc 198
 Val Gln Arg Gln Val Phe Ala Glu Asn Lys Asp Glu Ile Ala Leu Val

45 50 55

20 ctg ttt ggt aca gat ggc act gac aat ccc ctt tct ggt ggg gat cag 246
 Leu Phe Gly Thr Asp Gly Thr Asp Asn Pro Leu Ser Gly Gly Asp Gln

60 65 70

25 tat cag aac atc aca gtg cac aga cat ctg atg cta cca gat ttt gat 294
 Tyr Gln Asn Ile Thr Val His Arg His Leu Met Leu Pro Asp Phe Asp

75 80 85

ttg ctg gag gac att gaa agc aaa atc caa cca ggt tct caa cag gct 342
 Leu Leu Glu Asp Ile Glu Ser Lys Ile Gln Pro Gly Ser Gln Gln Ala

90	95	100	105	
gac ttc ctg gat gca cta atc gtg agc atg gat gtg att caa cat gaa				390
Asp Phe Leu Asp Ala Leu Ile Val Ser Met Asp Val Ile Gln His Glu				
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aca ata gga aag aag ttt gag aag agg cat att gaa ata ttc act gac				438
Thr Ile Gly Lys Lys Phe Glu Lys Arg His Ile Glu Ile Phe Thr Asp				
125 130 135				
10				
ctc agc agc cga ttc agc aaa agt cag ctg gat att ata att cat agc				486
Leu Ser Ser Arg Phe Ser Lys Ser Gln Leu Asp Ile Ile Ile His Ser				
140 145 150				
15				
ttg aag aaa tgt gac atc tcc ctg caa ttc ttc ttg cct ttc tca ctt				534
Leu Lys Lys Cys Asp Ile Ser Leu Gln Phe Phe Leu Pro Phe Ser Leu				
155 160 165				
20				
ggc aag gaa gat gga agt ggg gac aga gga gat ggc ccc ttt cgc tta				582
Gly Lys Glu Asp Gly Ser Gly Asp Arg Gly Asp Gly Pro Phe Arg Leu				
170 175 180 185				
25				
ggt ggc cat ggg cct tcc ttt cca cta aaa gga att acc gaa cag caa				630
Gly Gly His Gly Pro Ser Phe Pro Leu Lys Gly Ile Thr Glu Gln Gln				
190 195 200				
25				
aaa gaa ggt ctt gag ata gtg aaa atg gtg atg ata tct tta gaa ggt				678

	Lys Glu Gly Leu Glu Ile Val Lys Met Val Met Ile Ser Leu Glu Gly			
	205	210	215	
	gaa gat ggg ttg gat gaa att tat tca ttc agt gag agt ctg aga aaa 726			
5	Glu Asp Gly Leu Asp Glu Ile Tyr Ser Phe Ser Glu Ser Leu Arg Lys	220	225	230
	ctg tgc gtc ttc aag aaa att gag agg cat tcc att cac tgg ccc tgc 774			
	Leu Cys Val Phe Lys Lys Ile Glu Arg His Ser Ile His Trp Pro Cys			
10	235	240	245	
	cga ctg acc att ggc tcc aat ttg tct ata agg att gca gcc tat aaa 822			
	Arg Leu Thr Ile Gly Ser Asn Leu Ser Ile Arg Ile Ala Ala Tyr Lys			
	250	255	260	265
15	tcg att cta cag gag aga gtt aaa aag act tgg aca gtt gtg gat gca 870			
	Ser Ile Leu Gln Glu Arg Val Lys Lys Thr Trp Thr Val Val Asp Ala			
	270	275	280	
20	aaa acc cta aaa aaa gaa gat ata caa aaa gaa aca gtt tat tgc tta 918			
	Lys Thr Leu Lys Lys Glu Asp Ile Gln Lys Glu Thr Val Tyr Cys Leu			
	285	290	295	
	aat gat gat gat gaa act gaa gtt tta aaa gag gat att att caa ggg 966			
25	Asn Asp Asp Asp Glu Thr Glu Val Leu Lys Glu Asp Ile Ile Gln Gly			
	300	305	310	

	ttc cgc tat gga agt gat ata gtt cct ttc tct aaa gtg gat gag gaa		1014
	Phe Arg Tyr Gly Ser Asp Ile Val Pro Phe Ser Lys Val Asp Glu Glu		
315	320	325	
5	caa atg aaa tat aaa tcg gag ggg aag tgc ttc tct gtt ttg gga ttt		1062
	Gln Met Lys Tyr Lys Ser Glu Gly Lys Cys Phe Ser Val Leu Gly Phe		
330	335	340	345
10	tgt aaa tct tct cag gtt cag aga aga ttc ttc atg gga aat caa gtt		1110
	Cys Lys Ser Ser Gln Val Gln Arg Arg Phe Phe Met Gly Asn Gln Val		
	350	355	360
15	cta aag gtc ttt gca gca aga gat gat gag gca gct gca gtt gca ctt		1158
	Leu Lys Val Phe Ala Ala Arg Asp Asp Glu Ala Ala Ala Val Ala Leu		
	365	370	375
20	tcc tcc ctg att cat gct ttg gat gac tta gac atg gtg gcc ata gtt		1206
	Ser Ser Leu Ile His Ala Leu Asp Asp Leu Asp Met Val Ala Ile Val		
	380	385	390
25	cga tat gct tat gac aaa aga gct aat cct caa gtc ggc gtg gct ttt		1254
	Arg Tyr Ala Tyr Asp Lys Arg Ala Asn Pro Gln Val Gly Val Ala Phe		
	395	400	405
30	cct cat atc aag cat aac tat gag tgt tta gtg tat gtg cag ctg cct		1302
	Pro His Ile Lys His Asn Tyr Glu Cys Leu Val Tyr Val Gln Leu Pro		
	410	415	420
			425

ttc atg gaa gac ttg cgg caa tac atg ttt tca tcc ttg aaa aac agt	1350		
Phe Met Glu Asp Leu Arg Gln Tyr Met Phe Ser Ser Leu Lys Asn Ser			
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5			
aag aaa tat gct ccc acc gag gca cag ttg aat gct gtt gat gct ttg	1398		
Lys Lys Tyr Ala Pro Thr Glu Ala Gln Leu Asn Ala Val Asp Ala Leu			
445	450	455	
10 att gac tcc atg agc ttg gca aag aaa gat gag aag aca gac acc ctt	1446		
Ile Asp Ser Met Ser Leu Ala Lys Lys Asp Glu Lys Thr Asp Thr Leu			
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15 gaa gac ttg ttt cca acc acc aaa atc cca aat cct cga ttt cag aga	1494		
Glu Asp Leu Phe Pro Thr Thr Lys Ile Pro Asn Pro Arg Phe Gln Arg			
475	480	485	
20 tta ttt cag tgt ctg ctg cac aga gct tta cat ccc cgg gag cct cta	1542		
Leu Phe Gln Cys Leu Leu His Arg Ala Leu His Pro Arg Glu Pro Leu			
490	495	500	505
25 ccc cca att cag cag cat att tgg aat atg ctg aat cct ccc gct gag	1590		
Pro Pro Ile Gln Gln His Ile Trp Asn Met Leu Asn Pro Pro Ala Glu			
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gtg aca aca aaa agt cag att cct ctc tct aaa ata aag acc ctt ttt	1638		
Val Thr Thr Lys Ser Gln Ile Pro Leu Ser Lys Ile Lys Thr Leu Phe			

	525	530	535	
	cct ctg att gaa gcc aag aaa aag gat caa gtg act gct cag gaa att			1686
	Pro Leu Ile Glu Ala Lys Lys Lys Asp Gln Val Thr Ala Gln Glu Ile			
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	ttc caa gac aac cat gaa gat gga cct aca gct aaa aaa tta aag act			1734
	Phe Gln Asp Asn His Glu Asp Gly Pro Thr Ala Lys Leu Lys Thr			
	555	560	565	
10				
	gag caa ggg gga gcc cac ttc agc gtc tcc agt ctg gct gaa ggc agt			1782
	Glu Gln Gly Gly Ala His Phe Ser Val Ser Ser Leu Ala Glu Gly Ser			
	570	575	580	585
15				
	gtc acc tct gtt gga agt gtg aat cct gct gaa aac ttc cgt gtt cta			1830
	Val Thr Ser Val Gly Ser Val Asn Pro Ala Glu Asn Phe Arg Val Leu			
	590	595	600	
20				
	gtg aaa cag aag aag gcc agc ttt gag gaa gcg agt aac cag ctc ata			1878
	Val Lys Gln Lys Lys Ala Ser Phe Glu Glu Ala Ser Asn Gln Leu Ile			
	605	610	615	
25				
	aat cac atc gaa cag ttt ttg gat act aat gaa aca ccg tat ttt atg			1926
	Asn His Ile Glu Gln Phe Leu Asp Thr Asn Glu Thr Pro Tyr Phe Met			
	620	625	630	
	aag agc ata gac tgc atc cga gcc ttc cgg gaa gaa gcc att aag ttt			1974

	Lys Ser Ile Asp Cys Ile Arg Ala Phe Arg Glu Glu Ala Ile Lys Phe			
	635	640	645	
	tca gaa gag cag cgc ttt aac aac ttc ctg aaa gcc ctt caa gag aaa			2022
5	Ser Glu Glu Gln Arg Phe Asn Asn Phe Leu Lys Ala Leu Gln Glu Lys			
	650	655	660	665
	gtg gaa att aaa caa tta aat cat ttc tgg gaa att gtt gtc cag gat			2070
	Val Glu Ile Lys Gln Leu Asn His Phe Trp Glu Ile Val Val Gln Asp			
10	670	675	680	
	gga att act ctg atc acc aaa gag gaa gcc tct gga agt tct gtc aca			2118
	Gly Ile Thr Leu Ile Thr Lys Glu Glu Ala Ser Gly Ser Ser Val Thr			
	685	690	695	
15				
	gct gag gaa gcc aaa aag ttt ctg gcc ccc aaa gac aaa cca agt gga			2166
	Ala Glu Glu Ala Lys Lys Phe Leu Ala Pro Lys Asp Lys Pro Ser Gly			
	700	705	710	
20	gac aca gca gct gta ttt gaa gaa ggt ggt gat gtg gac gat tta ttg			2214
	Asp Thr Ala Ala Val Phe Glu Glu Gly Gly Asp Val Asp Asp Leu Leu			
	715	720	725	
	gac atg ata tag gtctggatg tatggggat ctaagagagc tgccatcgct			2266
25	Asp Met Ile			
	730			

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